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!!NA_SEQUENCE 1.0
ID    AI113131    standard; RNA; EST; 315 BP.
XX
AC    AI113131;
XX
SV    AI113131.1
XX
DT    04-SEP-1998 (Rel. 56, Created)
DT    15-MAR-1999 (Rel. 59, Last updated, Version 2)
XX
DE    UI-R-C2p-nr-f-06-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
DE    UI-R-C2p-nr-f-06-0-UI 3', mRNA sequence.
XX
KW    EST.
XX
OS    Rattus norvegicus (Norway rat)
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC    Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

XX
RN    [1]
RP    1-315
RX    MEDLINE; 97044477.
RA    Bonaldo M.F., Lennon G., Soares M.B.;
RT    "Normalization and subtraction: two approaches to facilitate gene
RT    discovery";
RL    Genome Res. 6(9):791-806(1996).
XX
CC    Contact: Soares, MB
CC    Program for Rat Gene Discovery and Mapping
CC    University of Iowa
CC    451 Eckstein Medical Research Building Iowa City, IA 52242, USA
CC    Tel: 319 335 8250
CC    Fax: 319 335 9565
CC    Email: msoares@blue.weeg.uiowa.edu
CC    Oligo-dT track not found, Not I site shown in beginning of sequence
CC    is likely internal to the message. cDNA Library Preparation: M.
CC    Fatima Bonaldo, Ph.D. Clone distribution: clones will be available

CC    through Research Genetics The following repetitive elements were
CC    found in this cDNA sequence: 97-125, >GC_rich#Low_complexity
CC    Seq primer: M13 Forward.
XX
FH    Key             Location/Qualifiers
FH
FT    source          1..315
FT                    /db_xref="taxon:10116"
FT                    /db_xref="ESTLIB:1413"
FT                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT                    polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
FT                    library is a subtracted library derived from the UI-R-C1
FT                    library, which is a subtracted library derived from the

FT                    UI-R-C0 library.  The UI-R-C0 library consisted of a
FT                    mixture of individually tagged normalized  libraries
FT                    constructed from rat placenta, adult lung, brain, liver,
FT                    kidney,  heart, spleen, ovary, muscle, 8, 12 and 18-day
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FT            bey      wen che Not I site and the  oligo-dT track which allow
FT            ide.tification of the library of origin of a clone within
FT            the mixture. The subtracted library (UI-R-C2p) was
FT            constructed as follows: PCR amplified cDNA inserts from

FT            UI-R-C1 clones from which 3' ESTs had been derived was us

FT            as a driver in a hybridization with the UI-R-C1 library i
FT            the form of single-stranded circles. The remaining
FT            single-stranded circles (subtracted library) was purified
FT            by hydroxyapatite column chromatography, converted to
FT            double-stranded circles and electroporated into DH10B
FT            bacteria (Life Technologies) to generate the UI-R-C2p
FT            library. This procedure has been previously described
FT            (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

FT            1996)"
FT            /organism="Rattus norvegicus"
FT            /strain="Sprague-Dawley"
FT            /clone="UI-R-C2p-nr-f-06-0-UI"
FT            /clone_lib="UI-R-C2p"
FT            /dev_stage="adult"
FT            /lab_host="DH10B (Life Technologies)"
XX
SQ    Sequence 315 BP; 46 A; 110 C; 116 G; 43 T; 0 other;

 Ai113131  Length: 315  March 20, 19100 09:52  Type: N  Check: 7433   ..

       1  CGGGCGCACG GTCTCAGGTC CGAAGTCCCT GAGCTCCGAC TGGTTGTTGA

      51  AGCGGGTGAG GCGCTTGCAC TTGCACGAGG CCACCATACG CACCTTGCGC

     101  GAGCGCCGCG CCGCGCCGCC GGGGCACAGC AGCTGCACCC GCTGCGCGCG

     151  GTAGCGATCC GGGATGCAGC GGAAGTCGGG TCCGTTCGGG CGCCACCACT

     201  TCACGCGCCC GATGGCGTTG GGCAGCAGCC GCGCGGGGCC GCACTGGCCC

     251  GAGCACACCA ACTCGGTGAC CGGCTTGGCA CTGCGGCACG GGCCGTCGGT

     301  CACGAAGCGG GTGTA
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!!NA_SEQUENCE 1.0
ID   HS1222641  standard; RNA; EST; 180 BP.
XX
AC   AA393939;
XX
SV   AA393939.1
XX
DT   19-MAY-1997 (Rel. 51, Created)
DT   19-MAY-1997 (Rel. 51, Last updated, Version 1)
XX
DE   zv64f09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
DE   758441 5'.
XX
KW   EST.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC   Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-180

RA   Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T

RA   Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K.
RA   Steptoe M., Tan F., Theising B., White Y., Wylie T., Waterston R.,
RA   Wilson R.;
RT   "WashU-Merck EST Project 1997";
RL   Unpublished.
XX
DR   RZPD; IMAGp998G181865Q6; 16-Jul-1999.
XX
CC   Contact: Wilson RK WashU-Merck EST Project Washington University
CC   School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC   MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC   est@watson.wustl.edu This clone is available royalty-free through
CC   LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for

CC   further information. Putative full length read The vector to vector
CC   length is Seq primer: -28m13 rev2 ET from Amersham.
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .180
FT                   /db_xref="taxon:9606"
FT                   /db_xref="ESTLIB:843"
FT                   /db_xref="RZPD:IMAGp998G181865Q6"
FT                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT                   polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT                   was prepared from mRNA obtained from pooled 8-9 week
FT                   (total) fetus material with a Not I - oligo(dT) primer [5'

FT                   TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3'].
FT                   Double-stranded cDNA was ligated to Eco RI adaptors
FT                   (Pharmacia), digested with Not I and cloned into the Not I
FT                   and Eco RI sites of the modified pT7T3 vector. Library wer
```

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. FT                      through one round of normalization, and was constructed
FT                        Bento Soares and M. Fatima Bonaldo."
FT                        /organism="Homo sapiens"
FT                        /clone="758441"
FT                        /clone_lib="Soares total fetus Nb2HF8 9w"
FT                        /dev_stage="8-9 weeks"

FT                        /lab_host="DH10B"
FT      mRNA              <1. .>180
XX
SQ      Sequence 180 BP; 61 A; 27 C; 55 G; 37 T; 0 other;
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Hs1222641 Length: 180 March 17, 19100 09:46 Type: N Check: 9094 ..

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    1 GAGAGAGAGA GAGAAAGAGA CTATTGGCAT ATGATTCCAA GGACTCCAGT

   51 GCCAGTTGAA TGGGCAGAGG TGAGAGAGAG AGAGAGAAAG AGAGAGAATG

  101 AATGCAGTTG CATTGATTCA GTGCCAAGGT CACTTCCAGA ATTCAGAGTT

  151 GTGATGCTCT CTTCTGACAG CCAAAGATGA
```

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ID    AC003098     standard; DNA; HUM; 94752 BP.
AC    AC003098;
SV    AC003098.1
DT    14-NOV-1997 (Rel. 53, Created)
DT    05-JUL-1999 (Rel. 60, Last updated, Version 11)
DE    Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.
KW    HTG.
OS    Homo sapiens (human)
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC    Primates; Catarrhini; Hominidae; Homo.
RN    [1]
RP    1-94752
RA    Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P., Lander E.;
RT    "Homo sapiens chromosome 17, clone HRPC905N1";
RL    Unpublished.
RN    [2]
RP    1-94752
RA    Birren B., Fasman K., McKernan K., Munro C., Nusbaum C., Richardson P.,
RA    Lander E., Baldwin J., Barna N., Cantu C., Chang A., Cooke P., Daly M.J.
RA    Devon K., Dewar K., DuRette B., Forrest C., Gage D., Gensheimer S.,
RA    Geraigery K., Gilmartin T., Hagos B., Halphen I., Harris K., Howland J.C
RA    Huang J., Hui L., Jacotot L., Kirby A., Lane M., MacKenzie J., Marquis N
RA    McDermott J., Molla M., Morrow J., Nachman A., Naylor J., O'Connor T.,
RA    Olotu A., Peterson K., Roberts D., Rollins G., Sarnaik A., Shiu P.,
RA    Shyam R., Stilwell J., Stone C., Strickland C., Sydney K., Tang L.,
RA    Zemtseva I., Zody M.;
RT    ;
RL    Submitted (10-NOV-1997) to the EMBL/GenBank/DDBJ databases.
RL    Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL    Cambridge, MA 02141, USA
RN    [3]
RP    1-94752
RA    Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P., Lander E.,
RA    Allen N., Baker J., Baldwin J., Barna N., Beckerly R., Boutwell C.,
RA    Byrne S., Cantu C., Castle A., Cooke P., Daly M.J., Depayre E., Devon K.,
RA    Dewar K., DuRette B., Etemadi S., Ferreira P., Forrest C., Gage D.,
RA    Gardyna S., Gensheimer S., Geraigery K., Gilmartin T., Gray D., Hagos B.,
RA    Harris K., Horton L., Howland J.C., Hui L., Jacotot L., Linton L.,
RA    MacKenzie J., Marquis N., McEwan P., McGurk A., Meldrim J., Molla M.,
RA    Morris W., Morrow J., Nachman A., Naylor J., O'Connor T., Pavlin B.,
RA    Peterson K., Ranganath S., Riley R., Roberts D., Rollins G., Rossello R.,
RA    Roy A., Shyam R., Soohoo S., Stilwell J., Stone C., Strickland C.,
RA    Sydney K., Tang L., Vassiliev H., Vo A., Wagner A., Wheeler J., Wu Y.,
RA    Ye W.J., Zemtseva I., Zhao J., Zody M.;
RT    ;
RL    Submitted (29-JAN-1998) to the EMBL/GenBank/DDBJ databases.
RL    Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL    Cambridge, MA 02141, USA
CC    All repeats were identified using RepeatMasker: Smit, A.F.A. &
CC    Green, P. (1996-1997) . . .
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SCORES   Init1: 10214   Initn: 10214   Opt: 10221 z-score: 3674.2 E():
99.4% identity in 2073 bp overlap

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Sa263085_000                            CTTTCGGTCATGATTCATTGTCTTTATTAA
                                        ||||||||||||||||||||||||||||||
Ac003098        CATGTGTGGTTGACAAAATGAGACCACATCCTTTCGGTCATGATTCATTGTCTTTATTAA
                   4230        4240        4250        4260        4270        4280


                2269        2259        2249        2239        2229        2219
Sa263085_000    CAATGTCTCTGGACTCTGGAAGAACAGACTGTTAATTCATAAAGCAATATTAACATTGTC

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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                   4290        4300        4310        4320        4330        4340


                2209        2199        2189        2179        2169        2159
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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                   4350        4360        4370        4380        4390        4400


                2149        2139        2129        2119        2109        2099
Sa263085_000    AACTCTTTAAAAACCACTACTTTCATTCTTGTGGACAAGTCCCACGTGGAAGAATTGCCA
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098        AACTCTTTAAAAACCACTACTTTCATTCTTGTGGACAAGTCCCACGTGGAAGAATTGCCA
                   4410        4420        4430        4440        4450        4460


                2089        2079        2069        2059        2049        2039
Sa263085_000    AAAAAACGACCAGTCCTGCAGGCTTTCATATGTCATGTGCTTCTGTTTAAAACTTTTTTT
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098        AAAAAACGACCAGTCCTGCAGGCTTTCATATGTCATGTGCTTCTGTTTAAAACTTTTTTT
                   4470        4480        4490        4500        4510        4520


                2029        2019        2009        1999        1989        1979
Sa263085_000    TTTTAACAATTAAAAACTACACAGAAAGTAAGAGGTTGTCTGGAAATGATTTTCAAAAAG
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098        TTTTAACAATTAAAAACTACACAGAAAGTAAGAGGTTGTCTGGAAATGATTTTCAAAAAG
                   4530        4540        4550        4560        4570        4580


                1969        1959        1949        1939        1929        1919
Sa263085_000    ATTTTTGGGTGGCAGCTATTATGCTCTGCAGTTTCTCAGCATATGTACAGCACTTGTAGT
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Ac003098        ATTTTTGGGTGGCAGCTATTATGCTCTGCAGTTTCTCAGCATATGTACAGCACTTGTAGT
                   4590        4600        4610        4620        4630        4640


                1909        1899        1889        1879        1869        1859
Sa263085_000    TTTTCCCCCAATAATATTCTTTTAGTGTAAGATATGCCATCACATGTAAGAGCAGTAAGA
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098        TTTTCCCCCAATAATATTCTTTTAGTGTAAGATATGCCATCACATGTAAGAGCAGTAAGA
                   4650        4660        4670        4680        4690        4700


                1849        1839        1829        1819        1809        1799
Sa263085_000    AGCTGTTTTCTAGGCAGAAATGTGTCCGTGAGTGGTGGGCAGAAGGCGGTGTCTCAAAAG
                ||I||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098        AGCTGTTTTCTAGGCAGAAATGTGTCCGTGAGTGGTGGGCAGAAGGCGGTGTCTCAAAAG
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                 1789        779      1769        1759         1749        1739
Sa263085_000  GGATGTGCTGGTCTGTGAGTTTGTGATGGCTGCTCCCTCGGGCCTGCAAGGCCAGTGTCC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GGATGTGCTGGTCTGTGAGTTTGTGATGGCTGCTCCCTCGGGCCTGCAAGGCCAGTGTCC
                 4770        4780        4790        4800        4810        4820


                 1729        1719        1709        1699        1689        1679
Sa263085_000  TTGAACCTTTCACTTCTCTTCGGAAGGTGACTTTAAAACATGGCTATGGGTCGGGGGAGG

              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TTGAACCTTTCACTTCTCTTCGGAAGGTGACTTTAAAACATGGCTATGGGTCGGGGGAGG
                 4830        4840        4850        4860        4870        4880


                 1669        1659        1649        1639        1629        1619
Sa263085_000  GATGCTGCTCTTTGGGAAGTTGGGGCGGATGTGATTTCTATCCCTCCCACCACCCTCGGA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GATGCTGCTCTTTGGGAAGTTGGGGCGGATGTGATTTCTATCCCTCCCACCACCCTCGGA
                 4890        4900        4910        4920        4930        4940


                 1609        1599        1589        1579        1569        1559
Sa263085_000  CCCTCTCCTTTTCTACCCCAATGGATGATGTTATTTCTTTGAGATGGAGGGGTGGAGGTA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCCTCTCCTTTTCTACCCCAATGGATGATGTTATTTCTTTGAGATGGAGGGGTGGAGGTA
                 4950        4960        4970        4980        4990        5000


                 1549        1539        1529        1519        1509        1499
Sa263085_000  GCCAAACATCCGGGGAAGCCAGGCTGGGAAGCAGCATAGCTTCTTCCAGGAGTTTGTCAG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GCCAAACATCCGGGGAAGCCAGGCTGGGAAGCAGCATAGCTTCTTCCAGGAGTTTGTCAG
                 5010        5020        5030        5040        5050        5060


                 1489        1479        1469        1459        1449        1439
Sa263085_000  CCGTAAATATGTCAGCCATAAATAGACTCTTTACTTTTTTTTTTCTGTTTGTTTTTCATC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCGTAAATATGTCAGCCATAAATAGACTCTTTACTTTTTTTTTTCTGTTTGTTTTTCATC
                 5070        5080        5090        5100        5110        5120


                 1429        1419        1409        1399        1389        1379
Sa263085_000  TTTGGCTGTCAGAAGAGAGCATCACAACTCTGAATTCTGGAAGTGACCTTGGCACTGAAT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TTTGGCTGTCAGAAGAGAGCATCACAACTCTGAATTCTGGAAGTGACCTTGGCACTGAAT

                 5130        5140        5150        5160        5170        5180


                 1369        1359        1349        1339        1329        1319
Sa263085_000  CAATGCAACTGCATTCATTCTCTCTCTTTCTCTCTCTCTCTCACCTCTGCCCATTCAA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CAATGCAACTGCATTCATTCTCTCTCTTTCTCTCTCTCTCTCACCTCTGCCCATTCAA
                 5190        5200        5210        5220        5230        5240


                 1309        1299        1289        1279        1269        1259
Sa263085_000  AAGGCACTGGAGTCCTTGGAATCATATGCCAATAGTCTCCTCGAGATCCTATTCCCACCT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Ac003098      AAGGCACTGGAGTCCTTGGAATCATATGCCAATAGTCTCCTCGAGATCCTATTCCCACCT
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Sa263085_000 CCACCCTCATTTTACAAAGTGGAAATTGAGGTCCCGAAGGAGAATTGTGTAGTTCAAGGT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     CCACCCTCATTTTACAAAGTGGAAATTGAGGTCCCGAAGGAGAATTGTGTAGTTCAAGGT
                5310       5320       5330       5340       5350       5360

                1189       1179       1169       1159       1149       1139
Sa263085_000 TACACAGCAAGTTAGTGGCAGAGCCAGGACTAGAAACCACATCTACAGTTGCCCCCAGTC

             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     TACACAGCAAGTTAGTGGCAGAGCCAGGACTAGAAACCACATCTACAGTTGCCCCCAGTC
                5370       5380       5390       5400       5410       5420

                1129       1119       1109       1099       1089       1079
Sa263085_000 TTGTGCTCTGGGCACGCCTCAGGCTTTCTGATGGGCAGCGAGGTGCAAGGGGGAATCTTA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     TTGTGCTCTGGGCACGCCTCAGGCTTTCTGATGGGCAGCGAGGTGCAAGGGGGAATCTTA
                5430       5440       5450       5460       5470       5480

                1069       1059       1049       1039       1029       1019
Sa263085_000 TCCAACTTTCTTAACCAGTCCCTGGACTTTCCCACTCCCACACCGCTCCCTTAAAACCCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     TCCAACTTTCTTAACCAGTCCCTGGACTTTCCCACTCCCACACCGCTCCCTTAAAACCCC
                5490       5500       5510       5520       5530       5540

                1009        999        989        979        969        959
Sa263085_000 AGGGCGGTGAAAATGCTTCCATTTCTGCCTCCTCTGAAGTGGGACCAGCAAAGGTAGGCG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     AGGGCGGTGAAAATGCTTCCATTTCTGCCTCCTCTGAAGTGGGACCAGCAAAGGTAGGCG
                5550       5560       5570       5580       5590       5600

                 949        939        929        919        909        899
Sa263085_000 GCCCCAGAGGCGGGGCTGCGTGGCTCAGTGTCTGTGACTCTCAATTCCCTCCCCTGCCCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     GCCCCAGAGGCGGGGCTGCGTGGCTCAGTGTCTGTGACTCTCAATTCCCTCCCCTGCCCC
                5610       5620       5630       5640       5650       5660

                 889        879        869        859        849        839
Sa263085_000 GTGGGACCCCTCAGCTGGCGGGCTGAGGGGGGCCTTGCCGGCGCCCGGGATTCCTCAGGG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     GTGGGACCCCTCAGCTGGCGGGCTGAGGGGGGCCTTGCCGGCGCCCGGGATTCCTCAGGG
                5670       5680       5690       5700       5710       5720

                 829        819        809        799        789        779
Sa263085_000 CCTGGAAGGTCTCAGCCCCCTGCCCTGGGTTGCAGGCATTTACAATGAAATATAAACAAT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     CCTGGAAGGTCTCAGCCCCCTGCCCTGGGTTGCAGGCATTTACAATGAAATATAAACAAT
                5730       5740       5750       5760       5770       5780

                 769        759        749        739        729        719
Sa263085_000 CAAACCACGCGCAGAGGACAGAAATGTGGGGCGCGGGTTCAGGGCCGGGGCGCCCGCCGG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098     CAAACCACGCGCAGAGGACAGAAATGTGGGGCGCGGGTTCAGGGCCGGGGCGCCCGCCGG
                5790       5800       5810       5820       5830       5840
```

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              709        699        689        679        669        659
  Sa263085_000 TGGGGAGGGGCGCGGGCGGGCTCTAGTAGGCGTTCTCCAGCTCGGCCTGGTTGGCTTTGG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     TGGGGAGGGGCGCGGGCGGGCTCTAGTAGGCGTTCTCCAGCTCGGCCTGGTTGGCTTTGG
              5850       5860       5870       5880       5890       5900

              649        639        629        619        609        599
  Sa263085_000 CGCTCCGGGCGCGGGGCCGCGGCTTCCGGCCCTTCTGCGGCCGAGCGGCCTCGGTCCCGA

               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     CGCTCCGGGCGCGGGGCCGCGGCTTCCGGCCCTTCTGCGGCCGAGCGGCCTCGGTCCCGA
              5910       5920       5930       5940       5950       5960

              589        579        569        559        549        539
  Sa263085_000 AGTCCTTGAGCTCCGACTGGTTGTGGAAGCGGGTGAGGCGCTTGCACTTGCACGAGGCCA
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     AGTCCTTGAGCTCCGACTGGTTGTGGAAGCGGGTGAGGCGCTTGCACTTGCACGAGGCCA
              5970       5980       5990       6000       6010       6020

              529        519        509        499        489        479
  Sa263085_000 CCAGGCGCACCTTGCGCGCGCGCGGCGCCTCACCACCGGGACACAGCAGCTGCACGCGCT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     CCAGGCGCACCTTGCGCGCGCGCGGCGCCTCACCACCGGGACACAGCAGCTGCACGCGCT
              6030       6040       6050       6060       6070       6080

              469        459        449        439        429        419
  Sa263085_000 GCGCGCGGTAGCGGTCGGGGATGCAGCGGAAGTCGGGCCCACTAGGTCGCCACCACTTGC
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     GCGCGCGGTAGCGGTCGGGGATGCAGCGGAAGTCGGGCCCACTAGGTCGCCACCACTTGC
              6090       6100       6110       6120       6130       6140

              409        399        389        379        369        359
  Sa263085_000 CGCGGCCGATGGCGTTGGGCAGCAGGCGCGCCGGGCCGCACTGGCCGGAGCACACCAGCT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     CGCGGCCGATGGCGTTGGGCAGCAGGCGCGCCGGGCCGCACTGGCCGGAGCACACCAGCT
              6150       6160       6170       6180       6190       6200

              349        339        329        319        309        299
  Sa263085_000 CGGTGACCGGCTTGGCGCTGCGGCACGGCCCATCGGTCACGTAGCGGGTGAAGTGCAGCT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Ac003098     CGGTGACCGGCTTGGCGCTGCGGCACGGCCCATCGGTCACGTAGCGGGTGAAGTGCAGCT
              6210       6220       6230       6240       6250       6260

              289        279        269        259        249        239
  Sa263085_000 CGCGGCAGCTGTACTCGGACACGTCTTTGGTCTCAAAGGGGTG-GTG-GGGAGGCCGCCC
               |||||||||||||||||||||||||| |||   |   | ||| | ||| ||| ||||||||
  Ac003098     CGCGGCAGCTGTACTCGGACACGTCTGTGG--AGAGAGGCGCGCGTGAGGGTGGCCGCCC
              6270       6280       6290       6300       6310       6320

              229        219        209        199        189        179
  Sa263085_000 TCCGTTCTCCGCCCGGTTCATGGTCTTGTTGTTCTCCAGCTCCGGTGGAGGCTCGGGGTA
               ||
  Ac003098     GCCTGGCCACCCCTGCCCTGGACCGGCCCGTCTCTCTCCACCCCAGCCCTGCTTTTGCCA
              6330       6340       6350       6360       6370       6380
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